

Search completed: February 17, 2005, 16:58:05  
Job time : 42 secs

A:Molecule type: mRNA  
A:Residues: 1-69 <SI>  
A:Cross-references: GB:M62972; NID:g157263; PIDN:AAA28476.1; PID:g157267  
C:Superfamily: DNA-directed RNA polymerase 132K polypeptide  
C:Keywords: DNA binding; nucleotidyltransferase; nucleus; transcription; zinc finger

C:Genetics:  
A:Gene: DmRP140  
A:Cross-references: FlyBase:FBgn0003276  
A:Introns: 8/1  
Matches 53; Conservative 39; Mismatches 78; Indels 96; Gaps 12;

Query Match 7.0%; Score 102; DB 2; Length 1176;  
Best Local Similarity 19.9%; Pred. No. 4.7;  
Matches 53; Conservative 39; Mismatches 78; Indels 96; Gaps 12;

Qy 21 YQSADPVGSRNTDNKEGFYISAKYNPSIGHFRKFSAEETPINGTSLTKVKVFLKKDGD 80  
Db 813 YRSYKSDENRKGQDENF-----EXPGRGTQC-----GM-RNAH 846  
Qy 81 ITKKDDFTRVAPGIDFQNNIISFGSGSIGYSMDGPRIELEAAAYQQFNPKNTDNDTNGE 140  
Db 847 YDKLDDGGIIAPGI-----RVSGDDVVIGKIT-----LPENDDELDSNTRK 888  
Qy 141 YYKH-----FALSRKDAMEDQYVVLKNDGITPNSLMV-----NTCY 177  
Db 889 FSKRDASTFLRNSETGTVDQMLTLNSEGYKFCKIRVRSVRIPQIGDKFASRHGQGTC- 947  
Qy 178 DITAEGVSF---VPYACAGIGADLLT-----IPKDLNLKF-AYGOKIGISY 219  
Db 948 -----GIQYQEDMAFTCEGLAPDIINHPAIRMTIGHLIECLQKLGSNKGEIGDAT 1002  
Qy 220 PI-----TPVSFAFIGGYHGVIQNK 240  
Db 1003 PFNDANNVQKISTFLOEYGVHLRGNE 1028

RESULT 13  
B70448  
3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) II - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C>Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C:Accession: B70448  
V:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.  
Nature 392, 353-358, 1998  
A>Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196666; PMID:9537320  
A:Accession: B70448  
A>Status: preliminary;  
A:Molecule type: DNA  
A:Residues: 1-415 <AO>  
A:Cross-references: UNIPROT:O67612; GB:AEO00752; NID:g2984021; PIDN:AAC07574.1; PID:g2984021  
C:Experimental source: strain VF5  
C:Genetics:  
A:Gene: fabF  
C:Function:  
A:Pathway: fatty acid biosynthesis  
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-protein]  
C:Keywords: acyltransferase; fatty acid biosynthesis  
F:23-410/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>  
F:165/Active site: Cys #status predicted

Query Match 6.9%; Score 101.5; DB 2; Length 415;  
Best Local Similarity 21.7%; Pred. No. 1.3;  
Matches 60; Conservative 32; Mismatches 73; Indels 111; Gaps 14;

Qy 62 INGTNSLTKKVFLKKDGDITKKDDFTRVAPGIDFQNLIISFGSG-----SIGVSMDDGP 116  
Db 7 ITGIGAVTPIGTGVKK-----FWENLVKVGSGVDYIKSNFPDEYVIP 48  
Qy 117 IELEAAAYQQFNPKN-TDNDTNGEGYYKHFALSR-KDAME----- 155  
Db 49 VKIAAEVKDFNPPEFMDDKKARKASRFVFQAIKAVKEALSDSGLLESEYDPYRVGVIGT 108

C/Accession: JE0219  
R;Reddy, G.R.; Sulsana, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.  
Biochem. Biophys. Res. Commun. 247, 636-643, 1998  
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the trib  
A;Reference number: JE0216; MUID:98321180; PMID:9647746



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QY 168 FMSLMVNTCYDITAEVGSFVPYACAGIGADLITIFKDLNLKFAVQKIGISYPTTPVSA 227
Db 168 DISLMLNACYDIDLMDPVPFVYVACAGITDLVSVINATNPKLSYQGKLGISYSINPEASI 227
QY 228 FIGGYHGVIGNKPEKIPVITPVVNLNDAPQTTSS-----ASVTLDVGVFGGEIGMRPTF 280
Db 228 FIGGHRVIGNEPKDI--ATSKVFTSSGNASSNAVSPASAILDVCHFGIEIGGRVFP 284

RESULT 6
JE0220
28k surface antigen 1 - Ehrlichia canis
C;Species: Ehrlichia canis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0220
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe
A;Reference number: JE0216; MUID:98321180; PMID:9647746
A;Accession: JE0220
A;Molecule type: DNA
A;Residues: 1-287 <RED>
A;Cross-references: UNIPROT:Q9ZGJ0; GB:AF062762; NID:g3327964; PIDN:AAC26721.1; PID:g3327964

Query Match 35.3%; Score 515.5; DB 2; Length 287;
Best Local Similarity 39.3%; Pred. No. 1.7e-34;
Matches 120; Conservative 47; Mismatches 95; Indels 43; Gaps 7;

QY 1 MNYKILVRGALISLMSILPQSPADPVGSRDNDKEGFIYSAKNPSISHRKFSAEET 60
Db 1 MNYKKTFTVALVLTSTFTIFIPYSPARASTHN----FTISGKMYTASHFGIFSACE- 56
QY 61 PINGTNSLTKKVFGEL--KKDGDITKDDFTRVAP-----GIDFQNNLISFGSGISGYSDMG 114
Db 57 ----EQSFTKVLVGLDQRLSHNIINNDTAKSLKVQNSYFKYKNNPPLGPAAGIYSGN 112
QY 115 PRIELEAAVQOFPNPKNTDNN-----DTDNGEYKHFALSRKDMED 155
Db 113 SRIELEVSHEIFDTKPNPNNLYNDSHKYCALSHGSHCSGDSGDMW-----TAKT 163
QY 156 QOVVVLKNDGITFMSLMVNTCYDITAEVGSFVPYACAGIGADLITIFKDLNLKFAVQGI 215
Db 164 DKFVLLKNEGLLDVSMANACYDITTEKMPFSPYICAGITDILLISMFETTONKISYQGL 223
QY 216 GISYPTTPVSAFPGYHGVIGNKPEKIPVITPVVNLNDAPQTTSSAVTLDVGVFGGEIG 275
Db 224 GLANTINSRVSVFAGGHFHKVIGNEFKGIFTLPLDGSNIKVQ-QSATVTLDVCHFGIEIG 282
QY 276 MRPTF 280
Db 283 SRPFF 287

RESULT 7
I39648
major surface protein 4 - Anaplasma marginale
C;Species: Anaplasma marginale
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39648
R;Oberle, S.M.; Barbet, A.F.
Gene 136, 291-294, 1993
A;Title: Derivation of the complete map4 gene sequence of Anaplasma marginale without cl
A;Reference number: I39648; MUID:94124017; PMID:8294020
A;Accession: I39648
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-282 <RES>
A;Cross-references: UNIPROT:Q07408; GB:L01987; NID:gl42174; PIDN:AAC36877.1; PID:gl42175
C;Genetics:
A;Gene: map4

Query Match 26.4%; Score 386.5; DB 2; Length 282;
Best Local Similarity 32.2%; Pred. No. 5.1e-24;
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Matches 96; Conservative 54; Mismatches 113; Indels 35; Gaps 9;
QY 1 MNYKIL----VRSALISLMSILPQSPADPVGSRDNDKEGFIYSAKNY---PSI 49
Db 1 MNYRELFTGSLSAATVCACSLLVSGAVVASPMSHEVASSEGVMGSGSPVGAAYSPAPFSV 60
QY 50 SHP--RKFSAEETPINGTNSLTKKVFGELKKDGDITKDDFTRVAPGIDFQNNLISFGSGS 107
Db 61 TSFDMRESSKETSIVRGYDKSIATI-----DVSVPANFSKGYTTFAFSKNLITSFDGA 113
QY 108 IGYSDMGPRIELEAAVQOFPNPKNTDNDNGEYKH-----FALSRSKDMEDQOYVVLK 162
Db 114 VGSLSGARVELASRYRF-----ATLADGGVAKSGAESLAITDANITENYFVVK 166
QY 163 NDGITFMSLMVNTCYDITAEVGSFVPYACAGIGADLITIFKDLNLKFAVQKIGISYPT 222
Db 167 IDEITNTSVMLNGCYDVLHTDLPVSPVACAGIGASFDVDSKQVTTKLAYRGKVGISYQFT 226
QY 223 PEVSATFIGGYHGVIGNKPEKIPVITPVVNLNDAPQTTSSAVTLDVGVFGGEIGMRPTF 280
Db 227 PEISLVAGGFYHGLFDESXYKDI PAHNSVKFSG---EAKASVKAKIAIDYGFNLGARFLF 281

RESULT 8
JE0221
28k surface antigen 2 - Ehrlichia canis
C;Species: Ehrlichia canis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0221
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe
A;Reference number: JE0216; MUID:98321180; PMID:9647746
A;Accession: JE0221
A;Molecule type: DNA
A;Residues: 1-133 <RED>
A;Cross-references: UNIPROT:O85360; GB:AF062762; NID:g3327964; PIDN:AAC26722.1; PID:g3327964

Query Match 15.6%; Score 227.5; DB 2; Length 133;
Best Local Similarity 41.4%; Pred. No. 1.6e-11;
Matches 59; Conservative 20; Mismatches 49; Indels 13; Gaps 4;

QY 1 MNYKILVRGALISLMSILPQSPADPVGSRDNDKEGFIYSAKNPSISHRKFSAEET 60
Db 1 MNCKKVTFTSALISSIYFLPNVSYNPNVYG--NSMYGNFYISGKYMPSVPHGIFSAEE- 57
QY 61 PINGTNSLTKKVFGELKKD--GDI-----TKDGDFTRVAPGIDFQNNLISFGSGISGYSDMG 114
Db 58 ----EKKKTTVVYGLKENWAGDAISSQSPDDNFTIRNYSFKYASNKFLGFAVAIGYSIGS 113
QY 115 PRIELEAAVQOFPNPKNTDNN 134
Db 114 PRIEVMSEYAFDVKQGNV 133

RESULT 9
I54668
heat resistant agglutinin 1 - Escherichia coli
C;Species: Escherichia coli
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I54668; I69133; I69134
R;Lutwyche, P.; Rupp, R.; Cavanagh, J.; Warren, R.A.; Brooks, D.E.
Infect. Immun. 62, 5020-5026, 1994
A;Title: Cloning, sequencing, and viscometric adhesion analysis of heat-resistant agglut
A;Reference number: I54668; MUID:95012721; PMID:7927783
A;Accession: I54668
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-264 <RES>
A;Cross-references: UNIPROT:Q46678; EMBL:U07174; NID:g463910; PIDN:AAC13751.1; PID:g463910
A;Accession: I69133
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
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